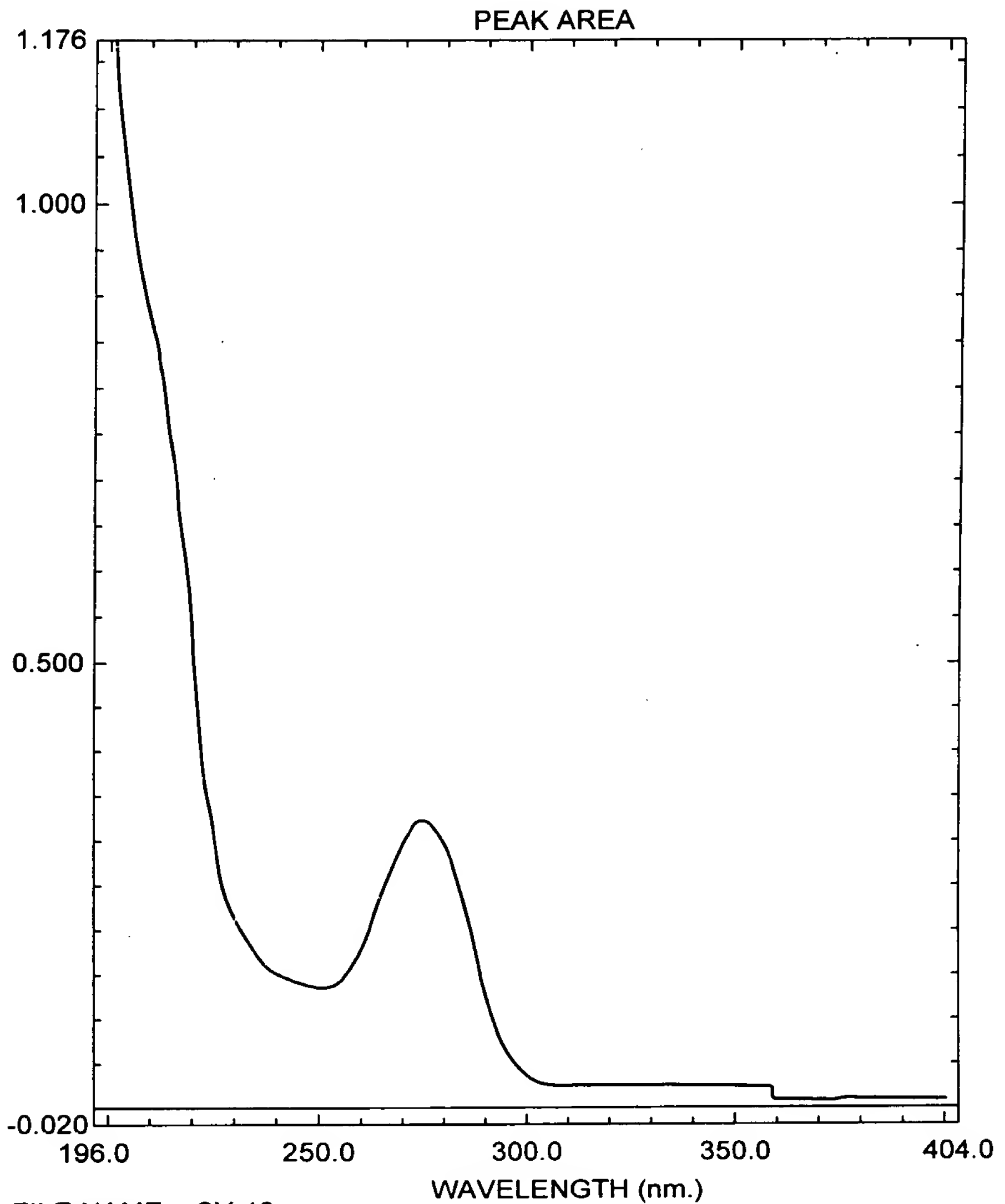


APPROVED	O.G. FIG.	
DRAFTSMAN	CLASS	SUBCLASS

09/881,569
U 013488-3



FILE NAME: SY-12

CREATED: 14:29 01-01-22

DATA: ORIGINAL

MEASURING MODE: ABS.

SCAN SPEED: FAST

SLIT WIDTH: 1.0

SAMPLING INTERVAL: 0.2

RESULT - (AREA-FACTOR) DIVISOR FACTOR = 9.999

REGION	START	END	DIVISOR	AREA	RESULT
--------	-------	-----	---------	------	--------

FIG. 1

208070" 69578860

APPROVED	O.G. FIG.	
DRAFTSMAN	CLASS	SUBCLASS

09/881,569
U 013488-3

C A M A G I L C Evaluation Software

ARBRO PHARMACEUTICALS LTD 6/14 KIRTI NAGAR INDUSTRIAL AREA NEW DELHI
PHONE: 5467228.515-0437. FAX: 91-11-5463784, E-mail: arbo@vsn1.com

TLC/HPTLC-Integration (CATS3.18 S/N:0207A004 / SCANNER I I V3.14 S/N:990602)

ESTIMATION OF L-LYSINE BY HPTLC

Calibr. Table Calibration Table created: ARBRO PHARMA LTD

File name: AMINO 3/JUN/0 14:49:46

Scan User name while measuring : ARBRO PHARMA LTD

File name: AMINO 3/JUN/0 14:54:52

INTEGRATION User while integrating: ARBRO PHARMA LTD

File name: AMINO 3/JUN/0 15:19:26

Track 1. Analysis a:

Peak #	start		max		end		area
	mm	h	mm	h	mm	h	
1	61.1	0.4	72.6	64.1	78.2	0.1	3186.2
				Total height =	64.1		
				Total area =	3186.2		
							100.00

Track 2. Standard level 1:

Peak #	start		max		end		area
	mm	h	mm	h [%]	mm	h	
1	62.9	2.8	71.0	63.5	78.8	0.0	3133.9
			Total height = 63.5		Total area = 3133.9		100.00

FIG. 2A

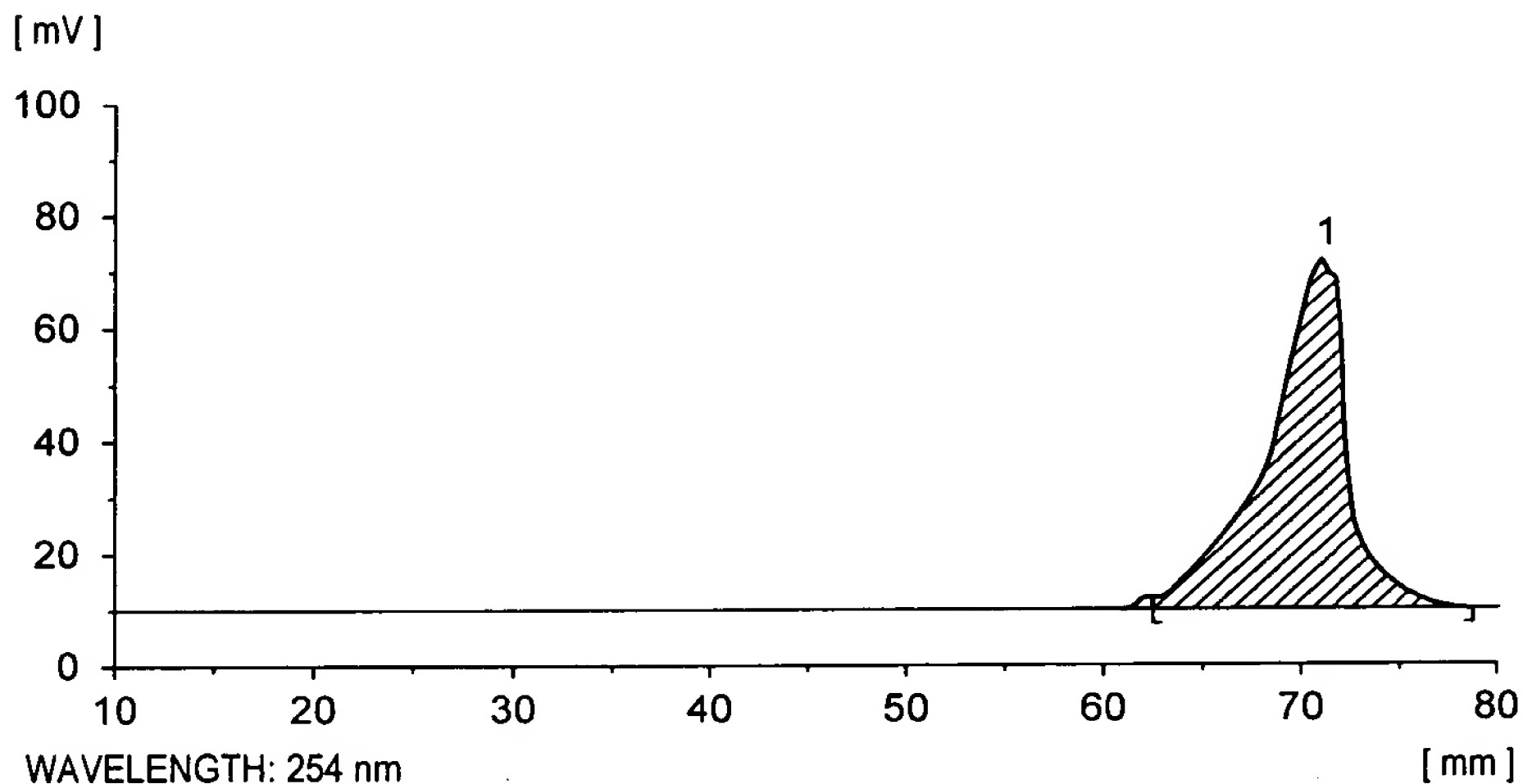
APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
GRAFTSMAN		

09/881,569
U 013488-3

CALIBRATION : H : AMINO ARBRO PHARMA LTD
METHOD SCAN INTEGRATION CALIBRATION DATA END

3/JUN/2000 15:05
HELP

STANDARD LEVEL 1



TRACK: 2, NOISE LEVEL: 0.108mV, RAW DATA FILE: AMINO
CATS3.18 S/N: 0207A004 CAMAG SOFTWARE (c) 1996 SCANNER II: 990602

TRACK 2. STANDARD LEVEL 1

PEAK #	START		MAX			END		AREA	
	mm	h	mm	h	[%]	mm	h	a	[%]
1	62.9	2.8	71.0	63.5	100.00	78.8	0.0	3133.9	100.00
TOTAL HEIGHT = 63.5					TOTAL AREA = 3133.9				

FIG. 2b

09881569-010802

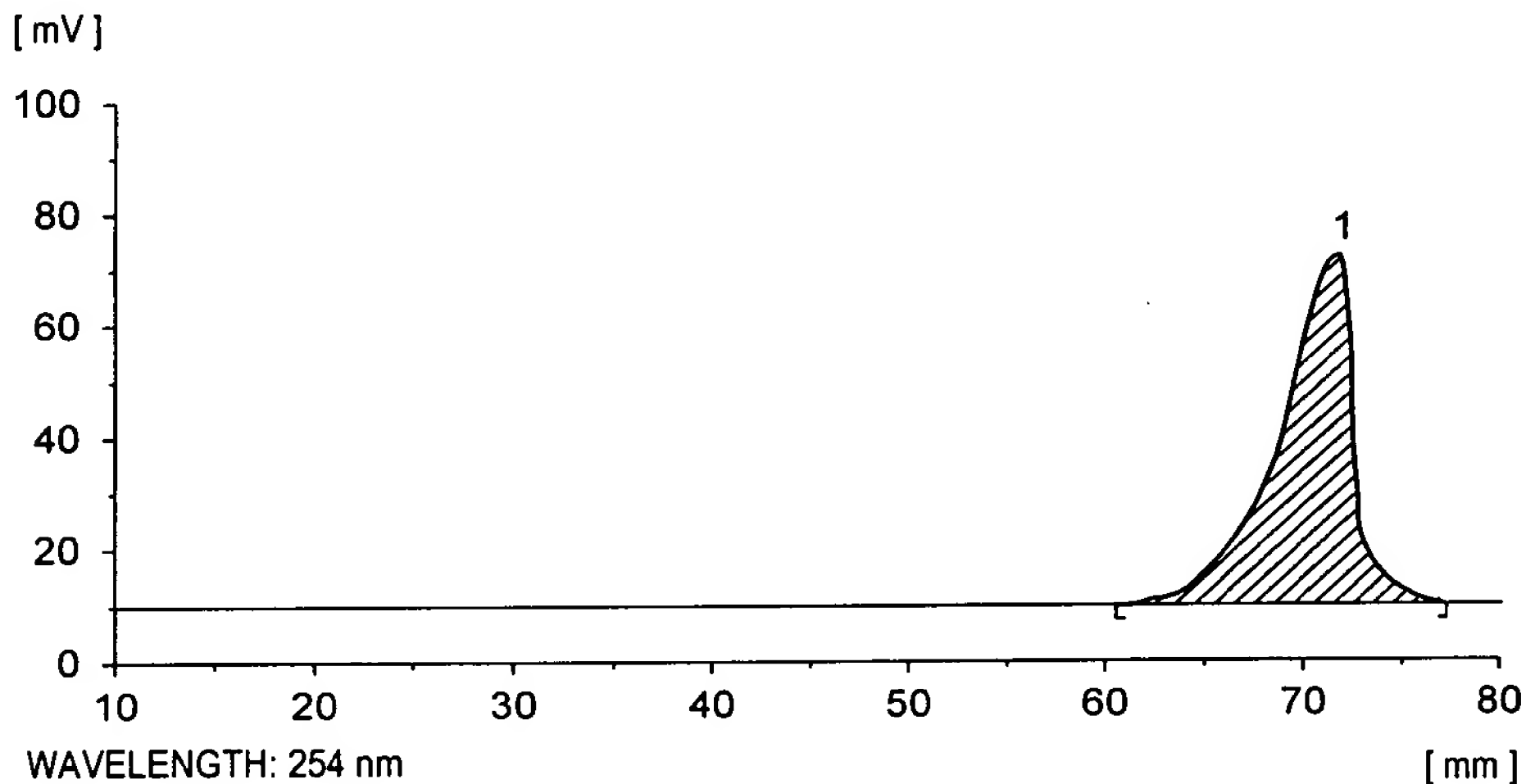
APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

09/881,569
U 013488-3

CALIBRATION : H : AMINO ARBRO PHARMA LTD
METHOD SCAN INTEGRATION CALIBRATION DATA END

3/JUN/2000 15:10
HELP

STANDARD LEVEL 1



TRACK: 1, NOISE LEVEL: 0.108mV, RAW DATA FILE: AMINO
CATS3.18 S/N: 0207A004 CAMAG SOFTWARE (c) 1996 SCANNER II: 990602

TRACK 1. ANALYSIS a:

PEAK #	START		MAX			END		AREA	
	mm	h	mm	h	[%]	mm	h	a	[%]
1	61.1	0.4	72.6	64.1	100.00	78.2	01	3186.2	100.00
TOTAL HEIGHT = 64.1					TOTAL AREA = 3186.2				

FIG. 2c

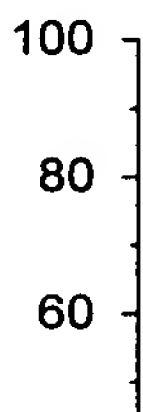
09881569-010802

APPROVED	D.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

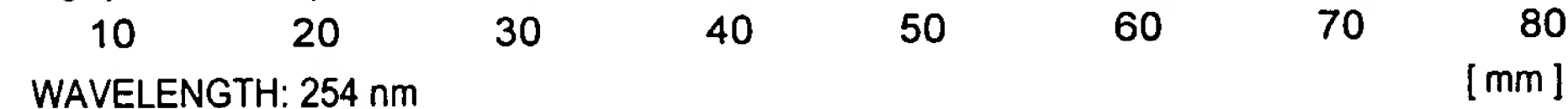
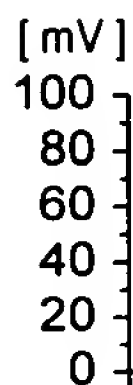
09/881,569
U 013488-3

CALIBRATION : H : AMINO ARBRO PHARMA LTD 3/JUN/2000 15:20
METHOD SCAN INTEGRATION CALIBRATION DATA END HELP

STANDARD LEVEL 1



CALIBRATION : H : AMINO ARBRO PHARMA LTD 3/JUN/2000 15:32
METHOD SCAN INTEGRATION CALIBRATION DATA END HELP



WAVELENGTH: 254 nm

FILE NAME : AMINO TRACK 1 TO 2
CATS3.18 S/N: 0207A004 CAMAG SOFTWARE (c) 1996 SCANNER II: 990602

FIG. 2d

09881569-010802

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

09/881,569
U 013488-3

SUBMITTER: PUSHPA KHANNA

SAMPLE NAME: GOURDIN

DATE:

	ASP	LEU				TYR		SER	HIS
		VAL	SER	GLN	GLN	VAL	GLY	GLN	ARG
SEQUENCE:	GLY	ILE	GLU	GLU	THR	THR		THR	LEU
CYCLE #:	1	2	3	4	5	6	7	8	9

		TYR	ARG				GLY		
	LYS	ILE	HIS	HIS	ASN	ARG	ASP	ARG	ARG
SEQUENCE:	ARG	LEU	ALA	GLU	ASP	ILE	LEU	THR	HIS
CYCLE #:	10	11	12	13	14	15	16	17	18

	SER							PRO	
	GLU		SER		GLU		THR	ARG	HIS
SEQUENCE:	LYS	ARG	PRO	ILE	LEU	PHE	SER	ALA	ARG
CYCLE #:	19	20	21	22	23	24	25	26	27

	GLY			VAL		PRO			
	VAL			LEU	ASN	ILE	ALA		
SEQUENCE:	ALA	GLY	ARG	ILE	SER	THR	VAL	ASN	
CYCLE #:	28	29	30	31	32	33	34	35	

YIELD(pmol): ILE(2) 98.11 YIELD(pmol): GLU(3) 56.13

CARRYOVER: ILE(6) 22.6% REP YIELD: ILE(2.23) 92.3%

SEQSTD YIELD: NL(6) 2.30 SEQSTD CARRYOVER: NL(6) 23.0%

SEQSTD REP YIELD: NL(6.11) 97.0%

COMMENTS: Mixtures with interchangeable amino acid at positions 12,13,15-19, 25-27 and 31-34.
Appears to be a mixture of sequences.

F I G. 3a

09881569-010302

2020T01695F3850

APPROVED	D.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

09/881,569
U 013488-3

GOURDIN PLANT

45.0

qt00-2637 32 (0.661) Cm (3:97)

4.0

TOF MS ES+
384

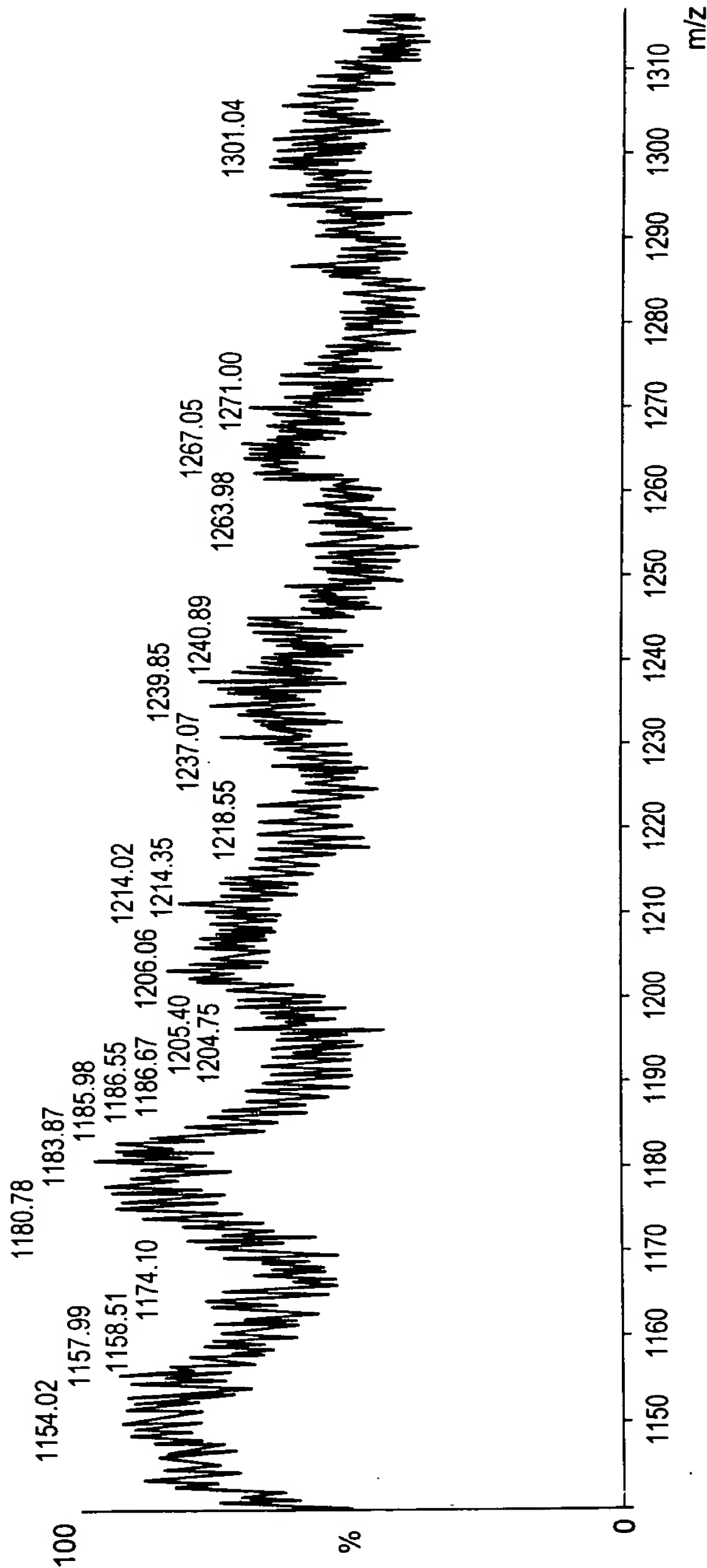


FIG. 4a1

208070" 69578860

VED	O.G. FIG.	
SHAN	CLASS	SUBCLASS

09/881,569
U 013488-3

GOURDIN PLANT

45.0

qt00-2637 32 (0.661) Sm (Mn, 2x3.00) Cm (3:97)

4.0

TOF MS ES+
345

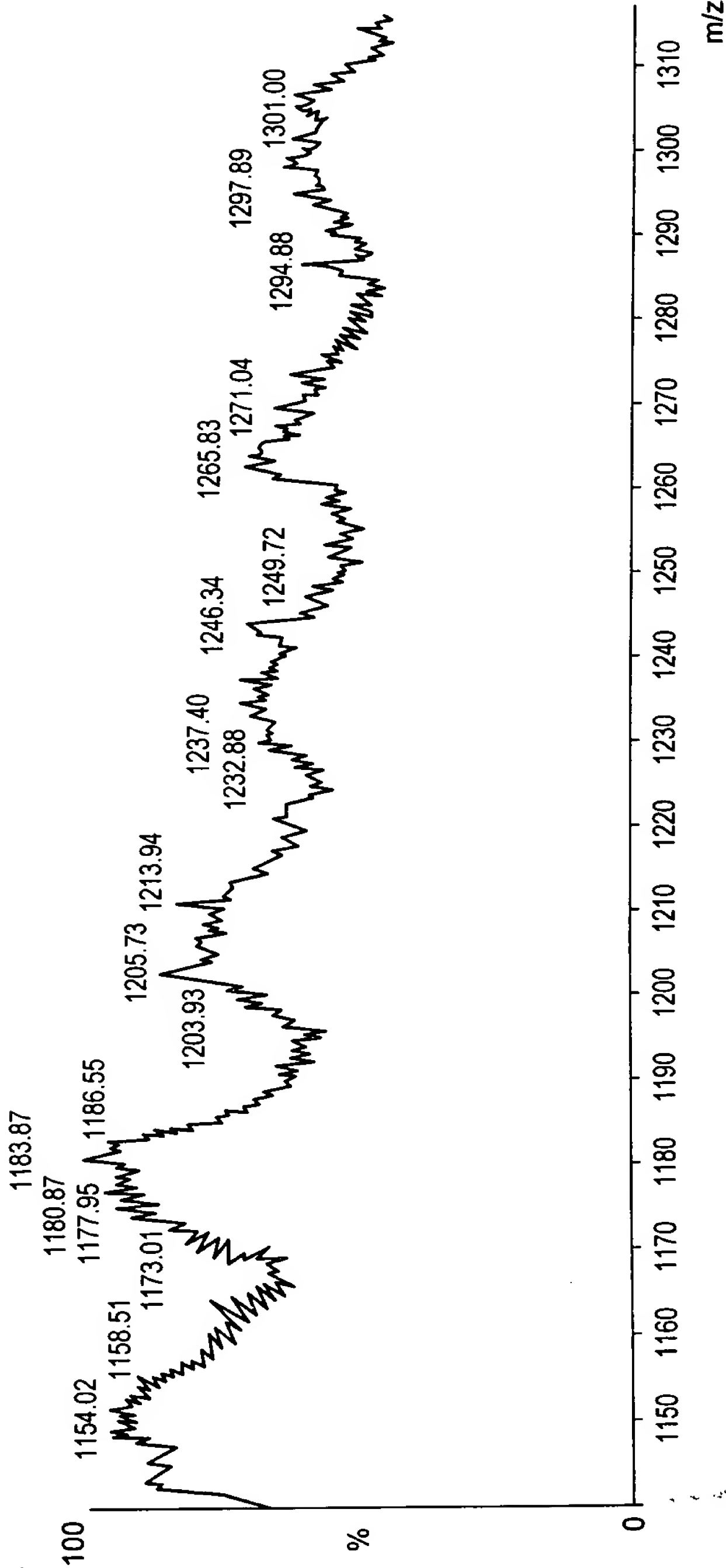


FIG. 4a2

2080T01 695T8860

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

09/881,569
U 013488-3

GOURDIN PLANT

45.0

qt00-2637 32 (0.661) Cm (3.97)

4.0

TOF MS ES+
555

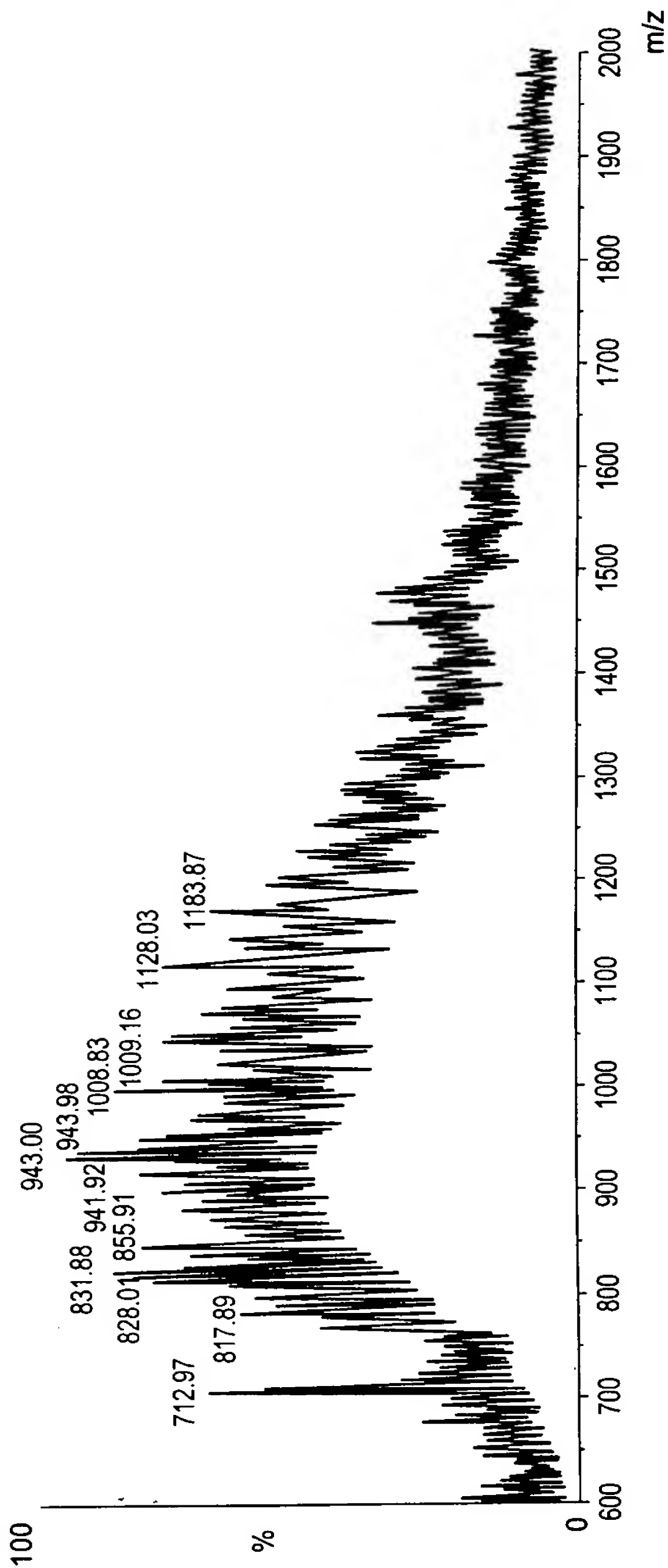


FIG. 4b1

208010-59518860

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

09/881,569
U 013488-3

GOURDIN PLANT

45.0

qt00-2637 32 (0.661) Sm (Mn, 2x3.00); Cm (3:97)

4.0

TOF MS ES+
501

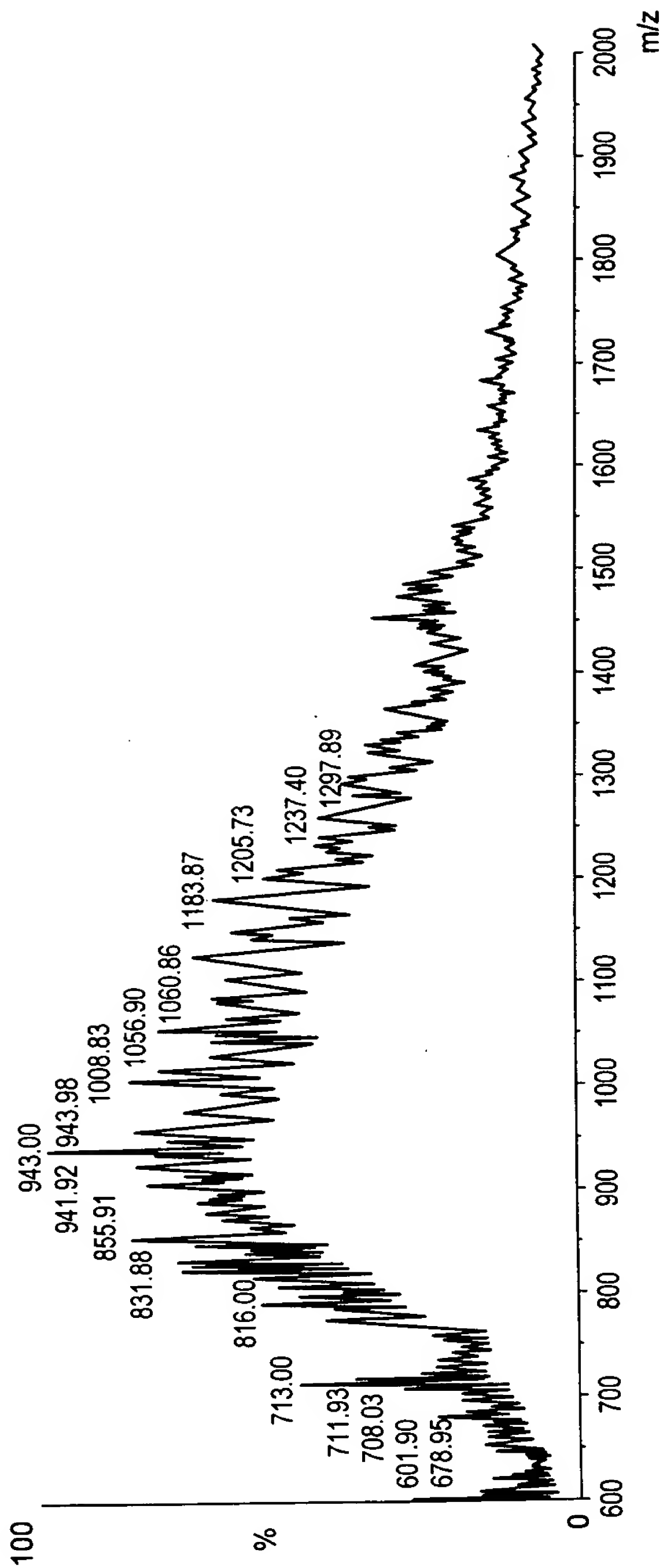
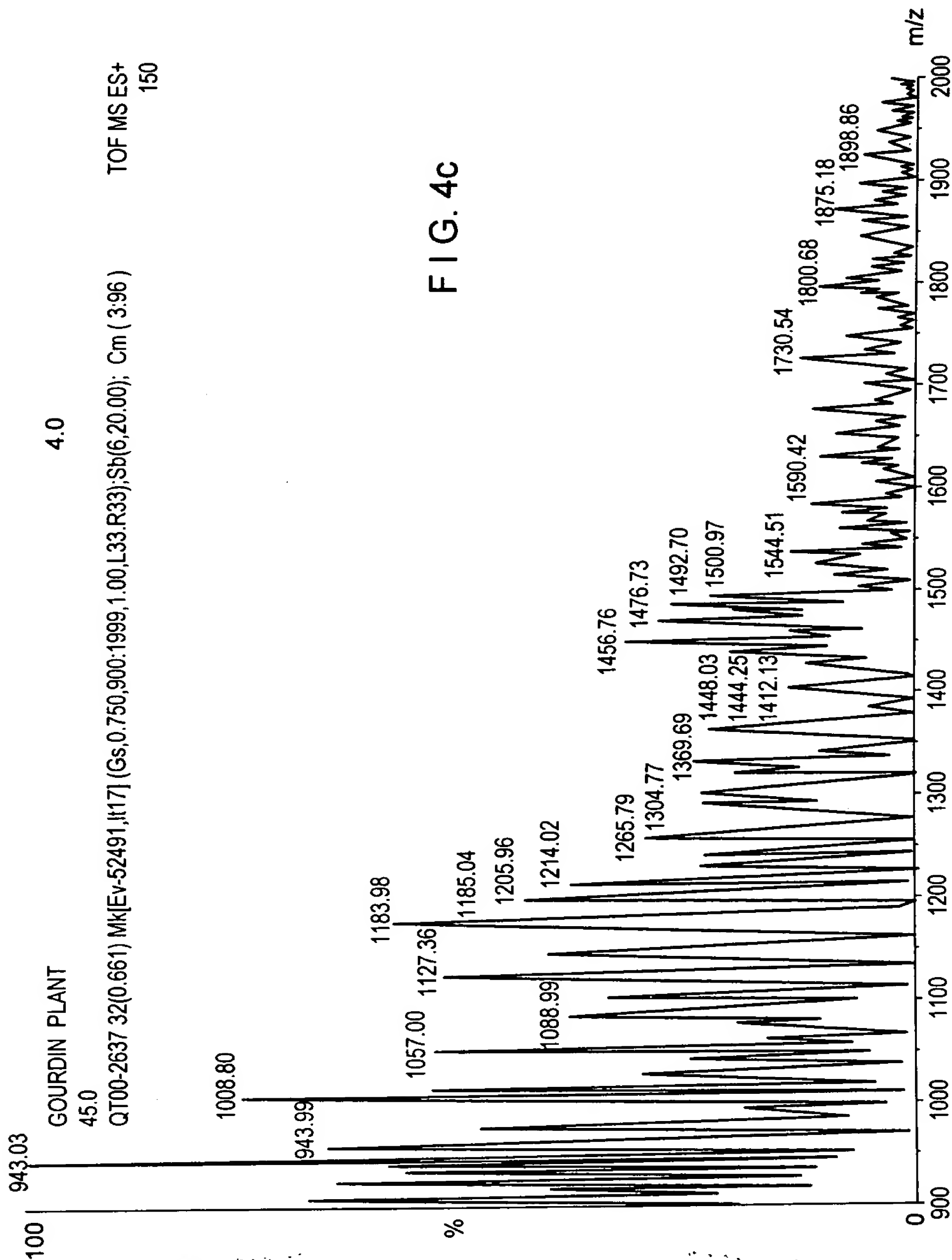


FIG. 4b2

208070 69578860

APPROVED	D.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

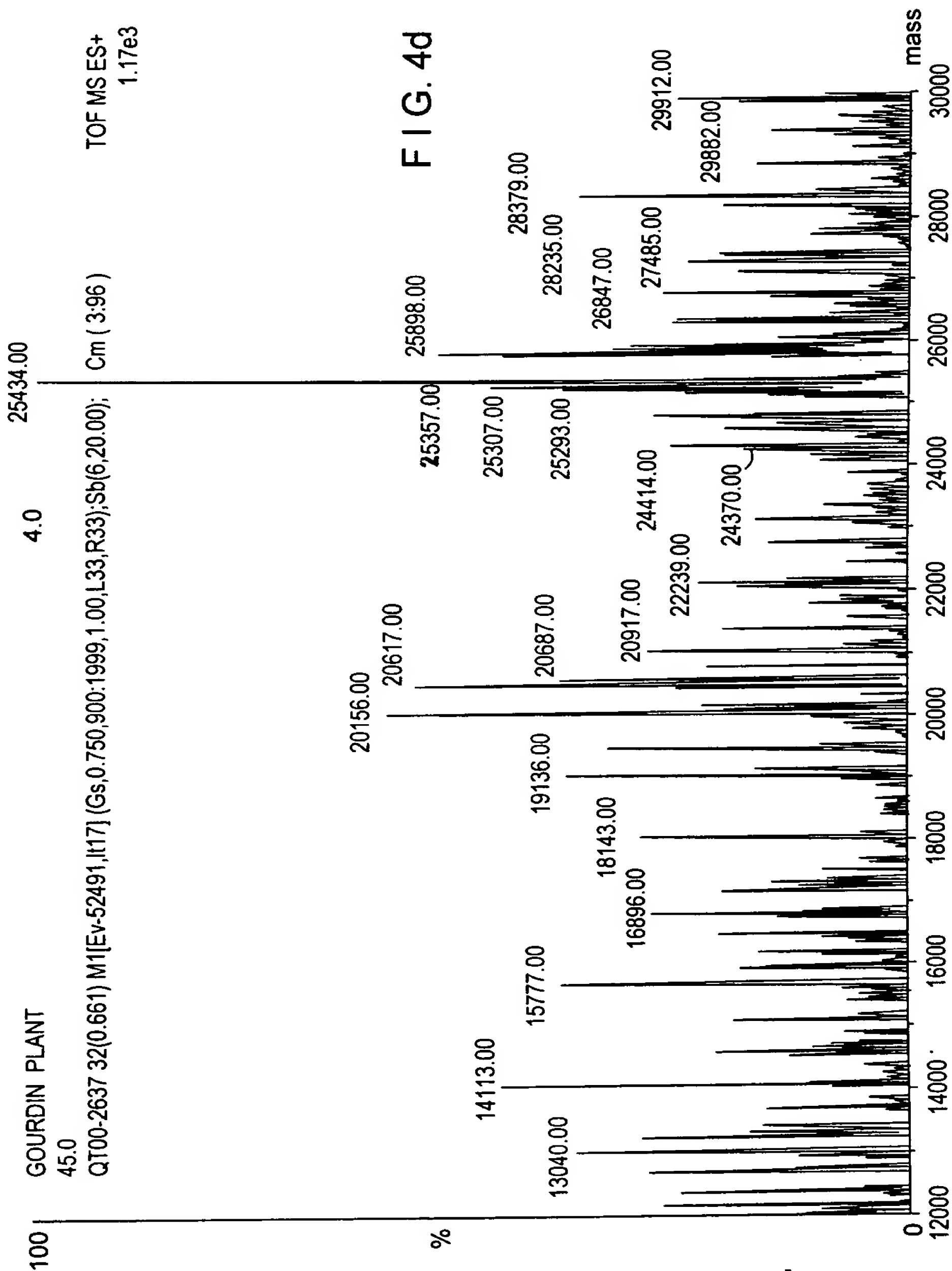
09/881,569
U 013488-3



2080 F0 695 F8860

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

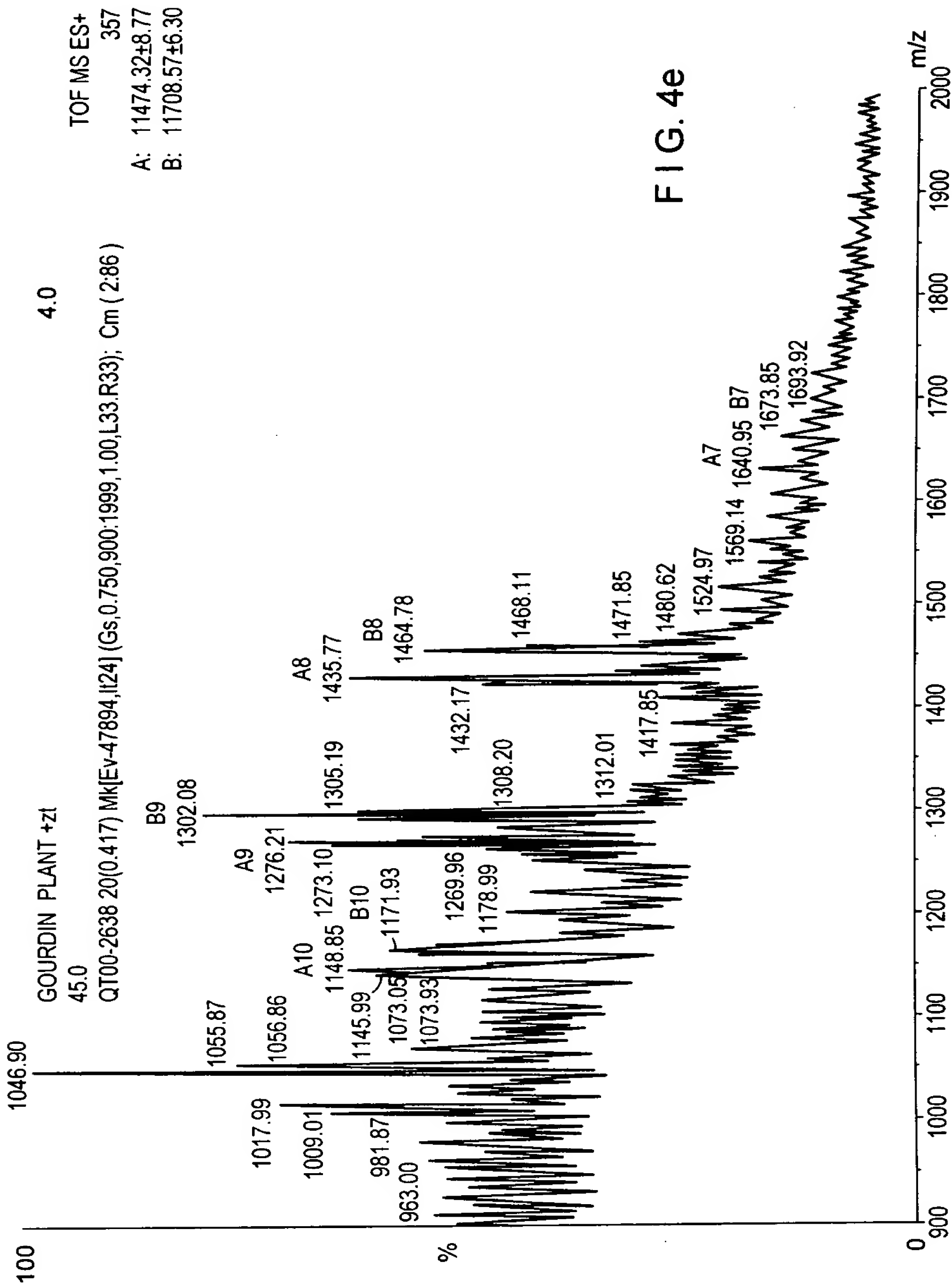
09/881,569
U 013488-3



2080T0 695T860

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

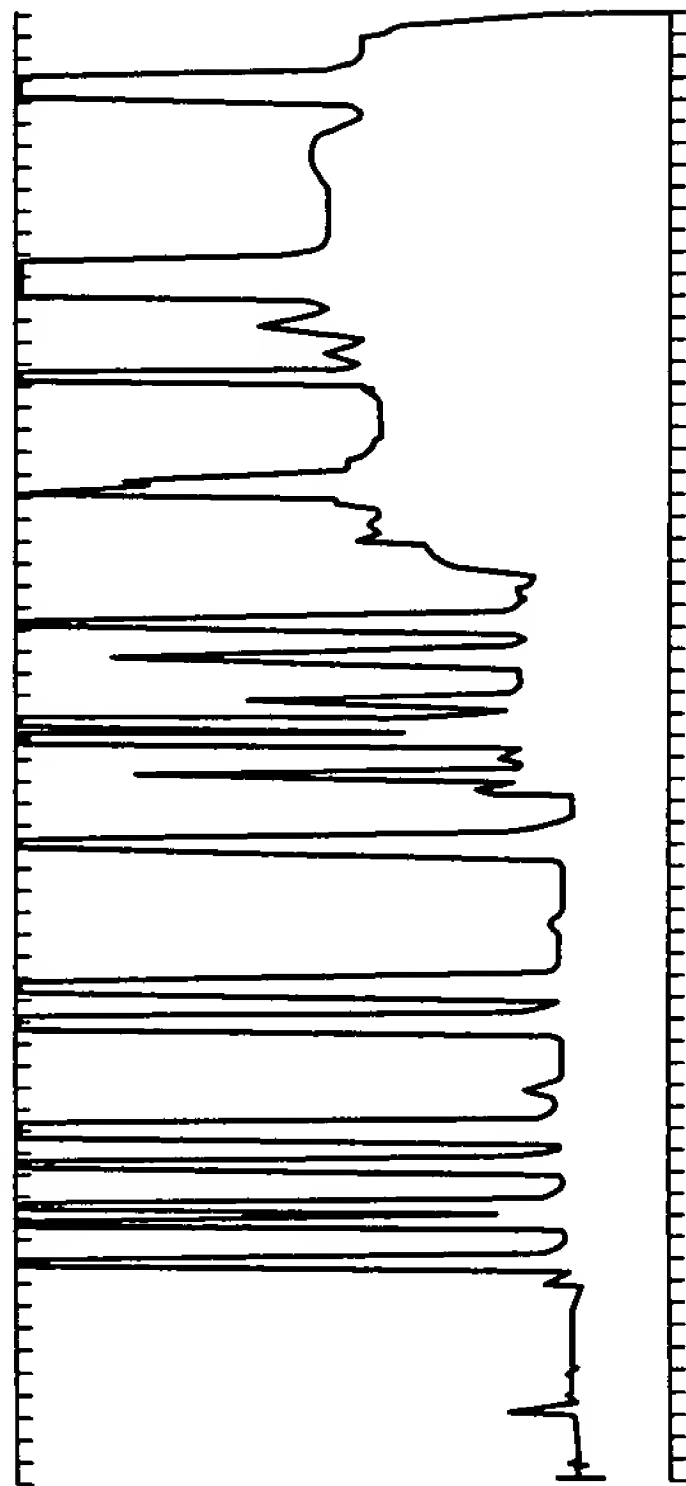
09/881,569
U 013488-3



208010 69578860

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

09/881,569
U 013488-3



INTERFACE 01 0-68 Min SCALE: 15 Mv Ch. A, 15 Mv Ch. B
AMINO ACID ANALYSIS PROCESSED: 11-22-2000 14:26:30, SEGMENT 17, CYCLE 936
RAW DATA SAVED IN FILE K: AAA936.PTS SECOND CHANNEL STORED IN K: BAA936.PTS

EXTERNAL STANDARD TABLE

***** 11-22-2000 14:26:30 Version 4.1 *****

Sample Name: amino acid analysis

Data File: K:AAA936

Date: 11-22-2000 14:26:30 Method: F:REBECKA

11-22-2000 13:54:21 #457

Interface: 0 Cycle #: 936 Operator jmc Channel #: 0

Vial #: N.A.

Starting Peak Width: 21 Threshold: .5 Area Threshold: 500

Starting Delay: 0.00

Ending retention time: 68.00

Area reject: 5000

One sample per: 2.002 sec.

Amount injected: 1.00

Dilution factor: 1.00

Sample weight: 1.000000

SEE FIG. 5a2

FIG. 5a1

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

09/881,569
U 013488-3

SEE FIG. 5a1

PEAK NUM	RET TIME	PEAK NAME	CONCENTRATION in nmoles	NORMALIZED CONC	AREA	HEIGHT	AREA/ HEIGHT	BL	REF PEAK	% DELTA RET TIME	CONC/ AREA
1	2.936			0.1504%	20695	1550	13.4	1	6	-1.592	3.4373E-06
2	8.609			0.0856%	9566	096	13.7	1	6	0	4.28185E-06
3	9.543	asx	3.6346	7.6853%	1019304	61489	16.6	1	6	.5811	3.5658E-06
4	11.378	thr	1.1549	2.4420%	314916	15245	20.7	2	6	.1132	3.6674E-06
5	12.112	ser	2.0456	4.3254%	595007	27668	21.5	2	6	0	3.4380E-06
6	14.081	int. std.	1.0397	2.1985%	576309	23599	24.4	2	6	0	1.0041E-06
7	15.649	glx	6.6195	13.9567%	1959672	71617	27.4	2	6	.1667	3.3779E-06
8	17.651	pro+ cys	2.1133	6.1414%	28161	809	34.8	2	6	-.2854	1.0314E-04
9	20.554	gly	3.4509	7.2968%	1098728	36599	30.0	2	9	0	3.1408E-06
10	22.256	ala	2.8168	5.9961%	801412	25276	31.7	2	9	0	3.5248E-06
11	28.996	val	2.6160	5.4358%	783543	16490	42.7	1	9	0	3.6541E-06
12	32.299	set	0.5625	1.1894%	157161	8772	17.9	1	16	.0101	3.5792E-06
13	33.166		0.0000	0.0000%	10132	523	19.4	1			0.0000E+00
14	33.967	ileu	1.8404	3.8914%	535119	23330	22.9	2	16	-.0931	3.4392E-06
15	34.735	leu	3.1701	6.7031%	953284	38035	25.1	2	16	0	3.3255E-06
16	35.902	nl-std.	6.2739	0.5791%	163238	6196	26.3	2	16	0	1.6777E-06
17	37.871	tyr	1.0645	2.2508%	290327	9412	30.8	1	16	0	3.6666E-06
18	39.473	phe	1.6115	3.4075%	408260	12881	31.7	1	16	0	3.9472E-06
19	45.479	his	1.2110	2.6711%	203562	8185	24.9	2	16	0	
20	46.013		0.0000	0.0000%	154147	5442	26.3	2			0.0000E+00
21	50.751	lys	1.2451	2.6327%	385456	13267	29.1	2	16	0	3.2302E-06
22	51.885			0.3929%	32441	913	35.5	2	16	0	5.7275E-06
23	53.287		0.0000	0.0000%	102408	2246	46.6	2			0.0000E+00
24	55.355	NH4	6.1666	13.0391%	3568874	61870	57.7	2	16	0	1.7279E-06
25	64.197	arg	3.5602	7.5279%	1016938	22156	45.9	1	16	0	3.5009E-06

TOTAL AMOUNT: 47.2934

FIG. 5a2

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

09/881,569
U 013488-3

AREAS, TIMES, AND HEIGHTS STORED IN : K: AAA936.ATB
DATA FILE = K: AAA936.PTS PRINTED ON 11-22-2000 AT 14:27:06
START TIME : 0.00 min. STOP TIME : 68.00 min. OFFSET : 0 mv
FULL RANGE : 15 millivolts

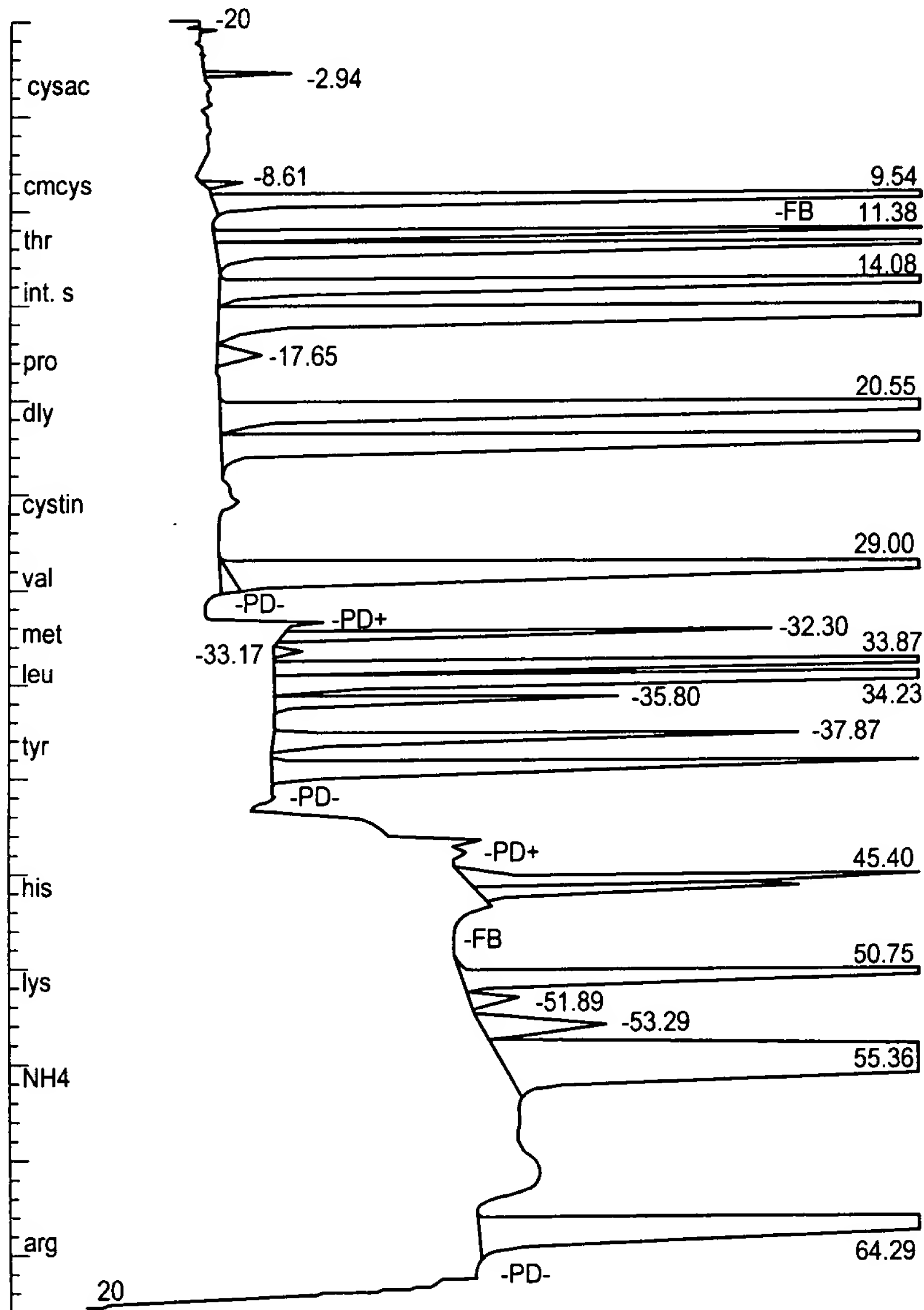


FIG. 5b

09/881,569-010802

203010" 69518860

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

09/881,569
U 013488-3

EXTERNAL STANDARD TABLE

***** 11-22-2000 14:28:43 Version 4.1 *****

Sample Name: amino acid analysis

Data File: K:BAA936

Date: 11-22-2000 14:26:30 Method: F:REBECKA

11-22-2000 13:55:21 #257

Interface: 0 Cycle #: 936 Operator jmc

Channel #: 1 Vial #: N.A.

Starting Peak Width: 21 Threshold: .5 Area Threshold: 500

Starting Delay: 0.00

Ending retention time: 68.00

Area reject: 5000

One sample per: 2.002 sec.

Amount injected: 1.00

Dilution factor: 1.00

Sample weight: 1.000000

PEAK NUM	RET TIME	PEAK NAME	CONCENTRATION in nmoles	NORMALIZED CONC	AREA	HEIGHT	AREA/ HEIGHT	BL	REF PEAK	% DELTA RET TIME	CONC/ AREA
1	8.775		0.0000	0.0000%	5143	286	18.0	1			0.0000E+00
2	9.510		0.0000	0.0000%	129394	7707	16.8	1			0.0000E+00
3	11.345		0.0000	0.0000%	24969	1171	21.3	2			0.0000E+00
4	12.079		0.0000	0.0000%	59106	2389	24.7	2			0.0000E+00
5	14.047		0.0000	0.0000%	47121	1978	23.8	1		.2393	0.0000E+00
6	15.616	glx	6.2317	74.6757%	375516	13802	27.2	1	7	0	1.6595E-05
7	17.651	pro+cys	(2.1133)	25.3244%	199944	6665	30.0	1	7		1.0570E-05
8	20.554		0.0000	0.0000%	83682	2753	30.4	1			0.0000E+00
9	22.222		0.0000	0.0000%	67237	2027	33.2	1			0.0000E+00

TOTAL AMOUNT: 8.3451

SEE FIG. 5c2

FIG. 5c1

2080TD" 695T8860

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

09/881,569
U 013488-3

SEE FIG. 5c1

AREAS, TIMES, AND HEIGHTS STORED IN: K: BAA936.ATB
DATA FILE = K: BAA936.PTS PRINTED ON 11-22-2000 AT 14:28:59
START TIME: 0.00 min. STOP TIME: 68.00 min. OFFSET: -95 mv
FULL RANGE: 15 millivolts

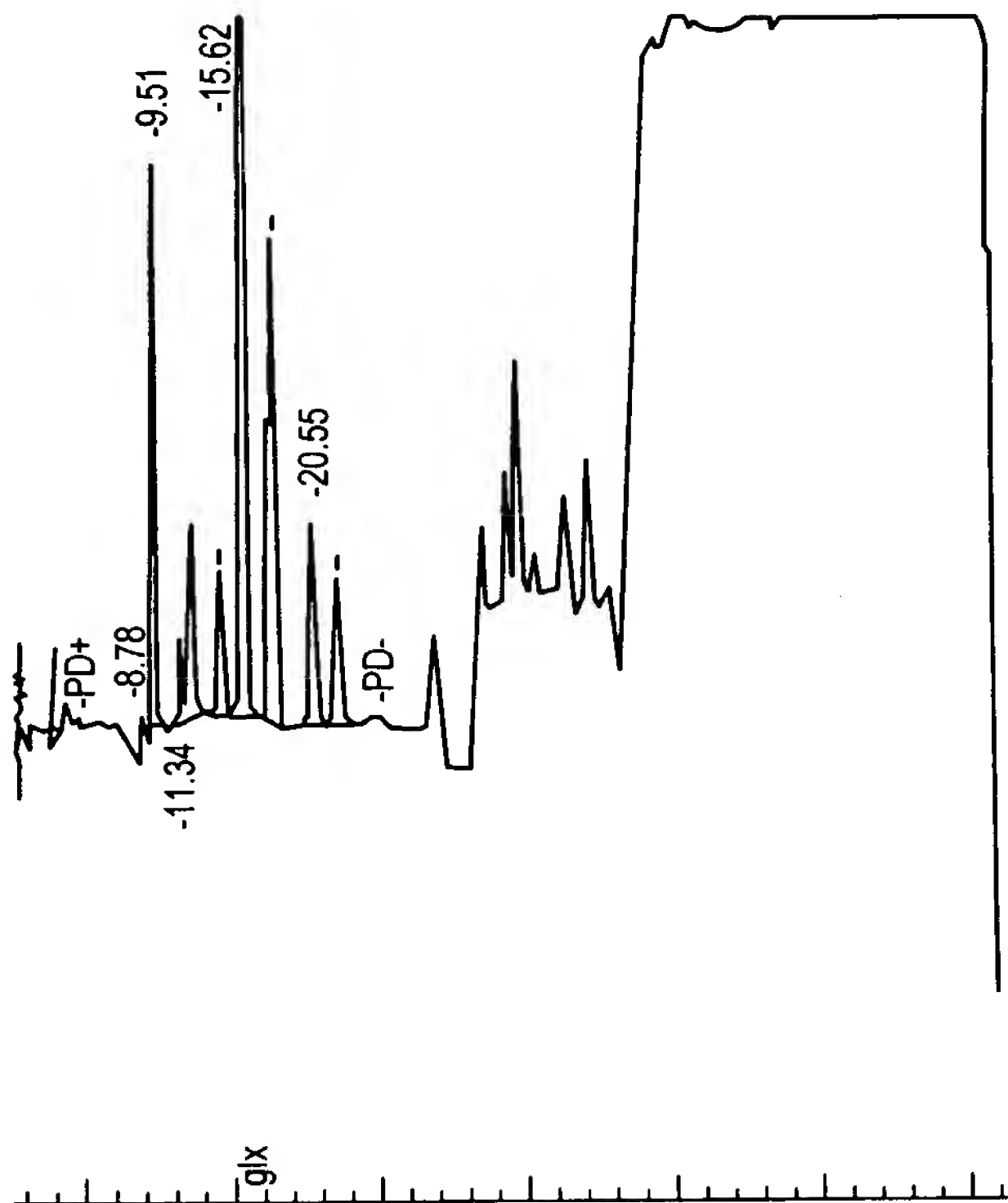


FIG. 5c2